

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17 : Search time 9 21:29 Seconds  
(without alignments)  
58.517 Million cell updates/sec

Title: US-09-856-070-26

Perfect score: 28

Sequence: 1 QDYEE 5

Scoring table: R10SNW62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134122 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	100.0	130	2 H84133	hypothetical prote
2	28	100.0	155	2 H83825	hypothetical prote
3	28	100.0	253	2 A01529	hypothetical prote
4	28	100.0	253	2 C98987	oxidoreductase (EC
5	28	100.0	315	2 A56561	35K proline-rich p
6	28	100.0	339	2 I08677	hypothetical prote
7	28	100.0	361	2 D95106	conserved hypothet
8	28	100.0	361	2 F97974	conserved hypothet
9	28	100.0	385	2 C75020	tryptophanyl-tRNA
10	28	100.0	432	2 I13476	hypothetical prote
11	28	100.0	443	2 I10891	GDP dissociation i
12	28	100.0	505	2 C72064	glutamyl-tRNA syn
13	28	100.0	505	2 F86560	glutamyl-tRNA syn
14	28	100.0	512	2 F92124	t-complex protein
15	28	100.0	568	2 T05060	hypothetical prote
16	28	100.0	575	2 A96766	unknown protein P2
17	28	100.0	581	2 I35889	serin bovine
18	28	100.0	586	2 A34400	serin bovine
19	28	100.0	630	2 T47177	hypothetical prote
20	28	100.0	700	2 F84131	transcription anti
21	28	100.0	811	2 T40276	probable glutamyl
22	28	100.0	961	2 H86181	hypothetical prote
23	28	100.0	1188	2 H86311	protein F113.20 [1
24	28	100.0	1263	2 I15196	hypothetical prote
25	25	89.3	65	2 F82547	hypothetical prote
26	25	89.3	82	2 F64308	hypothetical prote
27	25	89.3	93	2 F82775	hypothetical prote
28	25	89.3	97	2 A72346	hypothetical prote
29	25	89.3	99	2 A11786	hypothetical prote

30	25	89.3	105	2 H82407	hypothetical prote
31	25	89.3	113	2 I41691	hypothetical prote
32	25	89.3	127	2 A01529	hypothetical prote
33	25	89.3	127	2 A11171	hypothetical prote
34	25	89.3	129	2 A38221	hypothetical prote
35	25	89.3	131	2 B96782	unknown protein P2
36	25	89.3	132	2 I17907	hypothetical prote
37	25	89.3	134	2 A44173	calcitonin gene-re
38	25	89.3	141	2 F64033	hypothetical prote
39	25	89.3	146	2 A63065	hypothetical prote
40	25	89.3	162	2 D69439	conserved hypothet
41	25	89.3	187	2 B70658	conserved hypothet
42	25	89.3	187	2 H86974	probable efp prote
43	25	89.3	190	2 H83689	elongation factor
44	25	89.3	200	2 T06472	hypothetical prote
45	25	89.3	201	2 D86488	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

H84133

Hypothetical protein H83872 [imported] - Bacillus halodurans (strain C-125)

C.Species: Bacillus halodurans

C.Date: 01 Dec 2000 #sequence\_revision 01-Dec 2000 #text\_change 15-Jun-2001

C.Accession: H84133

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A.Reference numbers: A83650; MUID:29512582; PMID:11058132

A.Accession: H84133

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-130 <STO>

A.Cross-references: Jb.A061620; Gb.HA000004; NID:q10176401; PIRN:HA07591.1; GSPDB:G

A.Experimental source: strain C-125

C.Genetics:

A.Gene: BH3872

Query Match 100.0%, Score 28, DB 2, Length 130;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
|||||  
DB 81 QDYEE 85

##### RESULT 2

H83825

Hypothetical protein H81488 [imported] - Bacillus halodurans (strain C-125)

C.Species: Bacillus halodurans

C.Date: 01 Dec 2000 #sequence\_revision 01-Dec 2000 #text\_change 15-Jun-2001

C.Accession: H83825

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A.Reference numbers: A83650; MUID:29512582; PMID:11058132

A.Accession: H83825

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-156 <STO>

A.Cross-references: Gb.AB001611; Gb.HA000004; NID:q10176401; PIRN:HA07591.1; GSPDB:G

A.Experimental source: strain C-125

C.Genetics:

A.Gene: BH1408

Query Match 100.0%, Score 28, DB 2, Length 156;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5

Db 9 QVYEE 13  
|||||

# RESULT 3

A55223

hypothetical protein sp1569 [imported] - Streptococcus pneumoniae (strain T1634)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03 Aug-2001 #text\_change 24-Aug-2001

C:Accession: A55223

R:Jettellin, H.; Nelson, K.E.; Paulsen, K.E.; Read, T.D.; Peterson, S.; H

on, J.D.; Umayam, L.A.; White, G.; Salzborg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris,

A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MIM:21457209; PMID:11463916

A:Accession: A55223

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75478.1; EMBL:G1474414; GSPIB:GN00164; TIGR:

A:Experimental source: Strain 11064

C:Genetics:

A:Gene: SPI909

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 100.0%; Score 28; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 99 QVYEE 103

# RESULT 4

C98087

oxidoreductase (EC 1.1.1.1) [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence\_revision 22 Oct-2001 #text\_change 02 Nov-2001

C:Accession: C98087

R:Roskings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHull, B.S.; E

n, R.; LeBlanc, D.J.; Lee, L.N.; Leikowitz, E.J.; Lu, J.; Matsushima, P.; McAleen, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Hellido, M.; Zhao, G.; Zook, C.; Hultz, R.H.; Jaskunas, S.R.

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MIM:21459245; PMID:11544234

A:Accession: C98087

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <KUR>

A:Cross-references: GB:AE007317, EMBL:AA05528.1, FID:G1545434, GSPIB:GN00174

C:Genetics:

A:Gene: ydcG

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match 100.0%; Score 28; DB 2; Length 253;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 99 QVYEE 103

# RESULT 5

A56561

68K proline-rich protein xlanA - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 21 Jul-1995 #sequence\_revision 03 Aug-1995 #text\_change 21-Jul-2000

C:Accession: A56561; S27946

R:Reddy, B.A.; Kloc, M.; Etkin, L.D.

Mech. Dev. 39, 143-150, 1992

A:Title: The cloning and characterization of a localized maternal transcript in Xenop

A:Reference number: A56561; MIM:2143758; PMID:1284029

A:Accession: A56561

A:Molecule type: mRNA

A:Residues: 1-315 <RED>

A:Cross-references: EMBL:894959; NID:G214904; PIDN:AAA73357.1; FID:Q214905

A:Experimental source: oocyte

A:Note: sequence extracted from NPH backbone (NPHBP-12602)

C:Comment: mRNA encoding this protein is found in the animal pole of mature oocytes a

C:Superfamily: SH3 homology

F:260 367/Domain: SH3 homology <SH3>

Query Match 100.0%; Score 28; DB 2; Length 315;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 226 QVYEE 230

# RESULT 6

T08677

hypothetical protein DKPZp5642222.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 23-Jul-1999

C:Accession: T08677

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16469

A:Accession: T08677

A:Molecule type: mRNA

A:Residues: 1-339 <WAM>

A:Cross-references: EMBL:AL049945

A:Experimental source: fetal brain; clone DKPZp5642222

C:Genetics:

A:Note: DKPZp5642222.1

Query Match 100.0%; Score 28; DB 2; Length 339;

Best Local Similarity 100.0%; Pred. No. 102;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVYEE 5

|||||

Db 114 QVYEE 118

# RESULT 7

D95106

conserved hypothetical protein SP0921 [imported] - Streptococcus pneumoniae (strain T

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C:Accession: D95106

R:Jettellin, H.; Nelson, K.E.; Paulsen, K.E.; Read, T.D.; Peterson, S.; H

on, J.D.; Umayam, L.A.; White, G.; Salzborg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MIM:21457209; PMID:11463916

A:Accession: D95106

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75045.1; FID:Q14972395; GSPIB:GN00164; TIGR:

A:Experimental source: Strain 11064

C:Genetics:

A:Gene: SP0921

Query Match 100.0%; Score 28; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
DB 123 QDYEE 127

## RESULT 8

F97974 conserved hypothetical protein SP3822 (imported) - Streptococcus pneumoniae (strain 66)

C.Species: Streptococcus pneumoniae

C.Date: 22-Nov-2001 #sequence\_revision 22-Oct-2001 #text\_change 22 Oct 2001

C.Accession: F97974

R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; H

C, R.; LeBlanc, D.J.; Lee, L.R.; Lefkowitz, E.J.; Liu, J.; Matsushima, P.; McAbidin, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

T Bacteriol 183, 5709-5717, 2001

A.Authors: Yang, Y.; Youd Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.P.

A.Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A.Reference number: A97872; MUID:21424245; PMID:11544234

A.Accession: F97974

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-361 <KUR>

A.Cross-references: GR-AB007317; PIRN-ABK09426 1; PIR-Q1545423; CSF0R-0N00174

C.Genetics:

A.Cene: spr0822

Query Match 100.0%; Score 28; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
DB 123 QDYEE 127

## RESULT 9

C75020 tryptophanyl-tRNA synthetase (trps) PAB1111 - Pyrococcus abyssi (strain Orsay)

C.Species: Pyrococcus abyssi

C.Date: 20-Aug-1999 #sequence\_revision 29 Aug 1999 #text\_change 20 Aug 2000

C.Accession: C75020

R.Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A.Description: Pyrococcus abyssi genomic sequence; insights into archaeal chromosomal stru

A.Reference number: A75001

A.Accession: C75020

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-385 <KAW>

A.Cross-references: GR-A1248288; GR-A1098846; NID:q5458980; PIRN:CAH50601.1; PIR:q545911

A.Experimental source: strain Orsay

C.Genetics:

A.Cene: trps; PAB1111

C.Superfamily: mammalian tryptophan tRNA ligase, amino acid-tRNA ligase repeat homology

Query Match 100.0%; Score 28; DB 2; Length 385;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
DB 66 QDYEE 70

## RESULT 10

143476 hypothetical protein WPFP434052.1 human

C.Species: Homo sapiens (man)

C.Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000

C.Accession: T43476

R.Ansorge, W.; Winkler, H.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, December 1999

A.Reference number: 222518

A.Accession: T43476

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-432 <AAA>

A.Cross-references: EMBL:AL133598

A.Experimental source: adult testis; clone DKFZp434H052

C.Genetics:

A.Notes: WPFP434H052.1

C.Superfamily: human hypothetical protein WPFP434H052.1

Query Match 100.0%; Score 28; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
DB 379 QDYEE 383

## RESULT 11

T10801 GDP dissociation inhibitor GDI1 - Volvox carterii f. naqariensis

C.Species: Volvox carterii f. naqariensis

C.Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 26-May-2000

C.Accession: T10801

R.Reyser, K.; Fabry, S.

submitted to the EMBL Data Library, July 1999

A.Description: Identification and characterization of a lower plant Ypt/Rab guanine

A.Reference number: 217156

A.Accession: T10801

A.Status: preliminary; translated from GR/EMBL/DDRJ

A.Molecule type: mRNA

A.Residues: 1-443 <BEY>

A.Cross-references: EMBL:U62866; NID:q1572517; PIR:q1572518

A.Experimental source: strain HK10

C.Genetics:

A.Cene: GDI1

C.Function:

A.Description: inhibits dissociation of GDP from GTP binding proteins

C.Superfamily: human GTP dissociation inhibitor XAF-4

Query Match 100.0%; Score 28; DB 2; Length 443;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYEE 5  
DB 147 QDYEE 151

## RESULT 12

C72064 glutamate-tRNA ligase (EC 6.1.1.17) [similarity] - Chlamydomonas reinhardtii (strains

C.Species: Chlamydomonas reinhardtii [similarity] - Chlamydomonas reinhardtii

C.Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 03-Jun-2002

C.Accession: C72064; D81603

R.Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Glininger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999

A.Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A.Reference number: A72000; MUID:99206606; PMID:10192388

A.Accession: C72064

A.Molecule type: DNA

A.Residues: 1-505 <ARN>

A.Cross-references: GR-AB001640; GR-AB001640; NID:q478845; PIRN:AAU16700.1; PIR:q437

A.Experimental source: strain C7L029

R.Peadar, P.D.; Brunham, R.C.; Shen, C.; Gill, S.P.; Heideberg, J.F.; White, O.; Hicke

, C.; Jackson, P.; Gwin, M.; Nelson, W.; LeBoeuf, F.; Kohnen, J.; McCarthy, G.; Saizbo

Nucleic Acids Res. 28, 1397-1406, 2000

A.Title: Genome sequence of Chlamydia trachomatis M-10 and Chlamydia pneumoniae A839

A.Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: D81603  
A:Molecule type: DNA  
A:Residues: 1-505 <REA>  
A:Cross-references: GB:AE002180; GB:AE002161; NID:q7189117; PIDN:AAF38063.1; PID:q718912  
A:Experimental source: strain AP39, HL cells  
C:Genetics:  
A:Gene: gltX; C90190  
C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology  
C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae  
C:Date: 02 May 2001 #sequence\_revision 02 Mar 2001 #text\_change 23 Mar 2001  
C:Accession: D86560  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiura, H.  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20430449; PMID:10871362  
A:Accession: D86560  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-505 <STO>  
A:Cross-references: GB:BA000008; NID:q8978941; PIDN:BA000766.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: gltX  
C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology  
Query Match 100.0%; Score 28; DB 2; Length 505;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYEE 5  
DB 54 QYEE 58  
RESULT 14  
D86560  
glutamine-tRNA synthetase [imported] Chlamydomonas reinhardtii (strain J138)  
C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae  
C:Date: 02 May 2001 #sequence\_revision 02 Mar 2001 #text\_change 23 Mar 2001  
C:Accession: D86560  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiura, H.  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20430449; PMID:10871362  
A:Accession: D86560  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-505 <STO>  
A:Cross-references: GB:BA000008; NID:q8978941; PIDN:BA000766.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: gltX  
C:Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology  
Query Match 100.0%; Score 28; DB 2; Length 505;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYEE 5  
DB 54 QYEE 58  
RESULT 14  
F90124  
t complex protein eta S9 [imported] - Galliardia theta nucleomorph  
C:Species: nucleomorph Galliardia theta  
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24 May 2001  
C:Accession: F90124  
R:Krauss, S.; Zauner, S.; Frankoliz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reiter, R.  
Nature 410, 1091-1096, 2001  
A:Title: The highly reduced genome of an enslaved algal nucleus.  
A:Reference number: A99082; MUID:11423671; PMID:11323671  
A:Accession: F90124  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <DB>  
A:Cross-references: GB:AF084031; NID:q1379434; PIDN:AAK39691.1; GSPDB:GN00152  
C:Genetics:  
A:Gene: teph  
A:Map position: 4  
A:Genome: nucleomorph  
C:Keywords: nucleomorph  
Query Match 100.0%; Score 28; DB 2; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

```

Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 QDYEE 5
      |||||
DB      78 QDYEE 82

RESULT 15
T05060
Hypothetical protein M3E9_130 Arabidopsis thaliana
C:Species:Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision: 23-Apr-1999 #text_change 11-Jun 1999
C:Accession: T05060
R:Revs: M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Boelisel, J.; Mewes, H.W.; Ma
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15396
A:Accession: T05060
A:Molecule type: DNA
A:Residues: 1-568 <REV>
A:Cross-references: EMBL:AI022223
A:Experimental source: cultivar Columbia; BAC clone M3E9
C:Genetics:
A:Map position: 4
A:Annotations: 106/3; 339/2; 392/2
A:Note: M3E9_130

Query Match      100.0%; Score 28, DB 2; Length 568;
Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 QDYEE 5
      |||||
DB      157 QDYEE 161

Search completed: January 16, 2003, 16:57:54
Job time : 9.21429 secs

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Search completed: January 16, 2003, 16:57:54  
Job time : 9.21429 secs